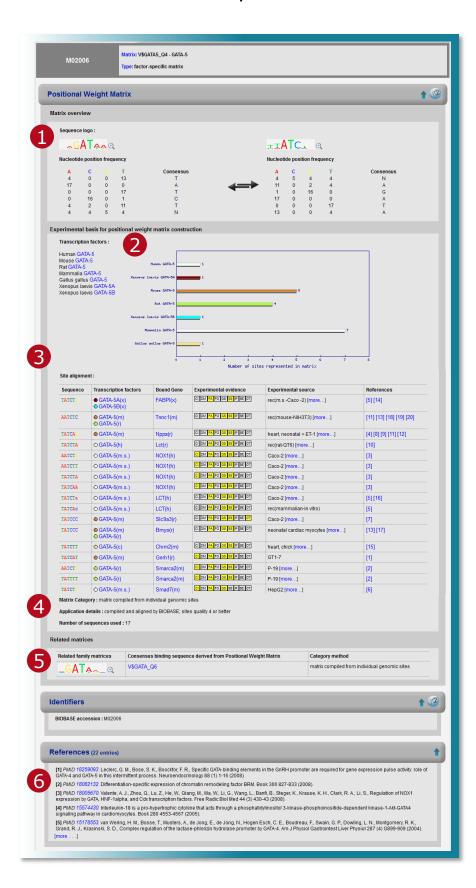
TRANSFAC® Matrix Report Overview





M02006: V\$GATA5 Q4



- The original and reverse complement nucleotide position frequency and sequence logo are both presented, making it easy to compare binding sites regardless of strand orientation.
- The new bar graph makes it easy to see at-a-glance how many binding sites each transcription factor contributed to the compiled matrix.
- The updated site alignment table provides (when applicable) detailed information for each of the binding sites used to compile the matrix including the binding factor, the bound gene, the experimental method and system used to determine binding, plus links to the reference(s) from which the site was taken.
- The new matrix category classification system (4) and related factor-specific and family matrices (5) allows you to easily identify how a matrix was constructed and to compare it to other matrices within TRANSFAC and public domain offerings.
- The reference section lists the complete set of supporting references.

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